



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/509,145

DATE: 10/05/2004

TIME: 10:53:57

Input Set : A:\82308.sequence

Output Set: N:\CRF4\10052004\J509145.raw

3 <110> APPLICANT: Epigenomics AG

5 <120> TITLE OF INVENTION: Method for the analysis of methylation patterns within  
nucleic acids

6 by means of mass spectrometry.

C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/509,145

C--> 8 <141> CURRENT FILING DATE: 2004-09-27

W--> 0 <130> FILE REFERENCE:

8 <160> NUMBER OF SEQ ID NOS: 3

10 <210> SEQ ID NO: 1

11 <211> LENGTH: 17

12 <212> TYPE: DNA

13 <213> ORGANISM: Homo Sapiens

15 <400> SEQUENCE: 1

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19 <210> SEQ ID NO: 2

20 <211> LENGTH: 18

21 <212> TYPE: DNA

22 <213> ORGANISM: Homo Sapiens

24 <400> SEQUENCE: 2

26 gcttggggga atagggag 18

28 <210> SEQ ID NO: 3

29 <211> LENGTH: 22

30 <212> TYPE: DNA

31 <213> ORGANISM: Homo Sapiens

33 <400> SEQUENCE: 3

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/509,145

DATE: 10/05/2004

TIME: 10:53:58

Input Set : A:\82308.sequence

Output Set: N:\CRF4\10052004\J509145.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No

L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE